c. of SEQ ID NO 3, beginning with the amino acid residue in any one of positions 1 to 5 and ending with the amino acid residue in any one of positions 40 to 104;

d. of SEQ ID NO 4, beginning with the amino acid residue in any one of positions 1 to 5 and ending with the amino acid residue in any one of positions 40 to 104; and

e. of SEQ ID NO 5, beginning with the amino acid residue in any one of positions 1 to 5 and ending with the amino acid residue in any one of positions 40 to 104.

REMARKS

Favorable reconsideration and allowance are respectfully requested. Claims 26-41 are pending and at issue.

Objection to the Specification

The Examiner objected to the specification for failing to provide a statement summarizing the priority information for the instant application. Accordingly, Applicants have amended page 1 of the specification to make reference to Application Nos. PCT/EP98/00294 and EP 97100883, as suggested by the examiner.

Rejection Under 35 U.S.C. § 112, Second Paragraph

Claims 26-41 were rejected under 35 U.S.C. § 112, second paragraph, as indefinite.

First, the Examiner required that the claims be amended to refer to an "isolated" or "purified" peptide. In addition, the Examiner rejected the claim because it uses the transitions "comprising" and "having", thereby encompassing a full-length protein. Accordingly, Applicants have amended claim 1 to refer to an "isolated peptide" in the preamble, and the claims now employ "consisting" as the transition, such that the claims do not encompass the full length protein.

Further, the Examiner objected to the term "homologous" because

> [i]t is unclear what level of homology is shared between the peptide and those peptides identified by SEQ ID NO. . . . [the] term . . . reads on a fragment which shares one amino acid in common . . . [and the] specification provides insufficient guidance as to what level of homology and characteristics define homologous. Office Action at 4.

Applicants respectfully disagree and direct the Examiner's attention to page 5, lines 1-3, of the specification, wherein the following definition of homologous is provided: "[t]he term 'homologous', as it is used in the present description and claims, refers to a sequence that is at least 80% identical to the respective sequence." Therefore, Applicants submit that it is quite clear what is meant by the term "homologous" and this basis for the Section 112, second paragraph rejection should be withdrawn.

Finally, the Examiner stated that claim 26 is vague and indefinite

> because it is unclear exactly what is being claimed. If Applicants intend to claim fragments of a polypeptide, then the exact fragment should be identified, i.e., an isolated polypeptide consisting of amino acids 1 to 40 of SEQ ID NO: 1. The claims is [sic] also vague and confusing because the preamble recites 'a peptide having 40 to 200 amino acid residues' while parts (a)-(e) only recite the longest peptide as 104 amino acid residues in length. This is extremely vague and confusing. What are the other 96 amino acid residues? Additionally, the recitation of beginning with any one of positions 1 to 5 and ending with any one of 40 to 104 does not limit the claim because open language is used. The peptide could encompass 1-600 amino acid residues and still anticipate the claim. Official Action at 4.

As discussed above, Applicants have amended claim 26 to refer to an *isolated* peptide *consisting of* 40 to 200 amino acid residues, wherein the sequence of that 40-200 residue peptide *comprises* an amino acid sequence having 40 or more amino acids that are identical or homologous to an amino acid sequence selected from the sequences identified in subparagraphs (a)-(e) of claim 26. Therefore, claim 26 is directed to an isolated peptide of 40-200 residues comprising a sequence identical or homologous to at least a portion of SEQ ID NOs 1-5.

Further, the Examiner appears to require clarification of subparagraphs (a)-(e) in claim 26. This section of the claim identifies that portion of the sequence set forth in SEQ ID NOs 1-5 which are included in sequence of the claimed peptide. For example, the claimed peptide may *comprise* a sequence selected from SEQ ID NO 1, wherein the first residue of that sequence corresponds to residue 1 of SEQ ID NO 1 and the last residue of that sequence corresponds to residue 104 of SEQ ID NO 1. Similarly, the claimed peptide may also comprise a sequence selected from SEQ ID NO 2, wherein the first residue of that sequence corresponds to residue 5 of SEQ ID NO 2 and the last residue of that sequence corresponds to residue 40 of SEQ

ID NO 2. Therefore, the claimed peptide consists of 40-200 residues, a portion of which comprises a sequence identical or homologous to the sequences identified in subparagraphs (a)-(e). Therefore, Applicants submit that the claims as amended sufficiently define the claimed invention and in view of the specification, the skilled artisan will readily appreciate the metes and bounds of the instant claims.

In view of the foregoing remarks and amendments, reconsideration and withdrawal of the Section 112, second paragraph rejection are respectfully requested.

Rejection Under 35 U.S.C. § 112, First Paragraph

Claims 26-41 were rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable the skilled artisan to make and/or use the claimed invention. In particular, the Examiner made the following observations:

> The specification states that substitutions, additions, or deletions may be made to the defined sequences; however, the specification provides no guidance as to what nucleotides may be changed without causing a detrimental effect to the protein/peptide to be produced. The specification provides insufficient guidance as to what level of homology and characteristics define homologous. Further, it is unclear how the amino acid sequence can vary without upsetting the function of the polypeptide. Official Action at 5.

Applicants respectfully disagree. First, as discussed above, the specification provides a definition of homology that clearly defines the metes and bounds of the instant specification. That definition is provided below:

> [t]he term 'homologous', as it is used in the present description and claims, refers to a sequence that is at least 80% identical to the respective sequence. . . . Similar amino acid sequences are aligned to obtain the maximum degree of homology. . . .
>
> Analogs of the peptide of the present invention accordingly are also within the scope of the present invention. An 'analog' peptide is an alternate form of a peptide that is characterized as having a substitution, deletion or addition of one or more amino acids that does not alter the biological function of the polypeptide. The biological function of the peptide of the present invention is eliciting a T-dependent immune response when used as [a] carrier together with an antigen. Specification at 5, lines 1-21.

Therefore, in view of the foregoing description in the subject specification, it will be clear to the skilled artisan that the claimed peptide should encompass a sequence that is identical or homologous to at least a portion of one or more of the sequences of SEQ ID NOs 1-5 and that the biological activity of the peptide should be maintained. It is well within the skill of the ordinary artisan to identify those modifications that will likely result in altered biological activity. For example, one would reasonably expect that the substitution of a glycine residue for an alanine residue (or vice versa) would not significantly affect the biological activity of a protein. Therefore, like substitutions or modifications are encompassed within the scope of the present invention. Further, as shown in the prior art references discussed below, the claimed peptide consists of sequences of known and well-characterized proteins, and the skilled artisan will readily appreciate what modifications would be tolerated.

Thus, Applicants submit that the instant claims are plainly enabled. Reconsideration and withdrawal of the Section 112, first paragraph rejection is therefore requested.

Rejections Under 35 U.S.C. § 102(b)

Claims 26-41 were rejected under 35 U.S.C. § 102(b) as anticipated by Lomholt et al., Pohlner et al., and Meyer et al. In particular, the Examiner noted that each of these references disclose the sequence of proteins that include fragments which are similar to SEQ ID NOs 1-5. Applicants respectfully traverse these rejections, addressed collectively below.

The instant claims relate to isolated peptides consisting of 40-200 amino acids, of which a portion corresponds to a sequence of an IgA1 protease from *Neisseria* or a homologous sequence (SEQ ID NOs 1-5). In contrast, the prior art of record discloses the full sequence of IgA1 protease from *Neisseria*, rather than the specific fragments of those sequences identified in the claims, and the prior art provides no guidance that would direct the skilled artisan to select the fragments corresponding to SEQ ID NOs 1-5 for inclusion in the peptides of the invention.

It is submitted that the cited prior art do not anticipate the claimed invention because the cited references do not direct the skilled artisan to select the instantly claimed fragment from the full sequence depicted in the references. An anticipatory reference must "clearly and unequivocally disclose the claimed compound or direct those skilled in the art to the compound without any need for picking, choosing, and combining various disclosures." *In re Arkley*, 455 F.2d 586, 587 (CCPA 1972). Therefore, absent a showing that clearly and unequivocally directs the skilled artisan to select the instantly claimed peptides from the full length sequences disclosed in the prior art, the cited references cannot be the basis for an anticipation rejection.

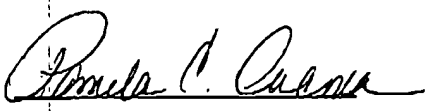
Thus, reconsideration and withdrawal of the anticipation rejections are respectfully requested.

Conclusion

In view of the foregoing amendments and remarks, Applicants submit that the claims are in condition for allowance and such action is earnestly solicited.

Respectfully submitted,

Dated: November 19, 2001



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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Mark ACHTMANN et al.

Serial No.: 09/142,970 Art Unit: 1645

Confirmation No.:

Filed: April 2, 1999 Examiner: J. Graser

For: IGA1 PROTEASE FRAGMENT AS CARRIER PEPTIDE

MARK-UP FOR AMENDMENT OF NOVEMBER 19, 2001
PURSUANT TO 37 C.F.R. § 1.121

Assistant Commissioner for Patents
Washington, DC 20231

IN THE SPECIFICATION:

At page 1, beneath the title of the application, please add the following paragraph:

--**Cross-Reference to Related Application(s)**

This application is a 371 of Application No. PCT/EP98/00294, filed January 20, 1998, which claims priority under 35 U.S.C. § 119(a)-(d) to Application No. EP 97100883.4, filed January 21, 1997.--

IN THE CLAIMS:

26 [A] An isolated peptide [having] consisting of 40 to 200 amino acid residues, wherein the peptide comprises an amino acid sequence having 40 or more amino acids that are identical or homologous to an amino acid sequence selected from the group consisting of amino acid sequences:

a. of SEQ ID NO 1, beginning with the amino acid residue in any one of positions 1 to 5 and ending with the amino acid residue in any one of positions 40 to 104;

b. of SEQ ID NO 2, beginning with the amino acid residue in any one of positions 1 to 5 and ending with the amino acid residue in any one of positions 40 to 104;

c. of SEQ ID NO 3, beginning with the amino acid residue in any one of positions 1 to 5 and ending with the amino acid residue in any one of positions 40 to 104;

d. of SEQ ID NO 4, beginning with the amino acid residue in any one of positions 1 to 5 and ending with the amino acid residue in any one of positions 40 to 104; and

e. of SEQ ID NO 5, beginning with the amino acid residue in any one of positions 1 to 5 and ending with the amino acid residue in any one of positions 40 to 104.

Respectfully submitted,

Dated: November 19, 2001

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